What is claimed:

1. An isolated variant of a G_q protein that exhibits increased promiscuity relative to the corresponding Gq protein.

2. The variant G_q protein of claim 1, wherein the G_q protein is of a subclass selected from the group consisting of $G\alpha_q$, $G\alpha_{11}$, $G\alpha_{14}$, and $G\alpha_{15}/G\alpha_{16}$.

3. The variant G_q protein of claim 2, wherein said G_q protein is of the $G\alpha_q$ subclass.

4. The variant G_q protein of claim 3, wherein said variant comprises at least one point mutation that increases promiscuity.

5. The variant G_q protein of claim 4, wherein said mutation is a Glycine to Aspartic acid change at position 66.

6. The variant G_q protein of claim 1, wherein said variant G_q protein is derived from a mammalian G_q protein.

7. The variant G_q protein of claim 6, wherein said mammalian G_q protein is derived from a mouse G_q protein.

8. The variant G_q protein of claim 6, wherein said mammalian G_q protein is derived from a human G_q protein.

9. The variant G_q protein of claim 1, wherein at least about five amino acids in the C terminus of said G_q protein are replaced by at least about five amino acids from the C terminus of $G\alpha_{olf}$ or transducin, and wherein said C-terminal substitution increases promiscuity of said variant G_q protein as compared to the corresponding native G_q protein.

10. The variant G_q protein of claim 9, wherein said variant G_q protein further comprises at least one point mutation that acts in addition to said C-terminal substitution to increase promiscuity of said variant G_q protein as compared to the corresponding native G_q protein.

11. A G_q chimeric protein comprising at least about five amino acids from the C terminus of transducin, wherein said chimeric protein has binding specificity for olfactory GPCRs and taste GPCRs.

12. A G_q chimeric protein comprising at least about five amino acids from the C terminus of $G\alpha_{olf}$, wherein said chimeric protein has binding specificity for olfactory GPCRs and taste GPCRs.

13. An isolated $G\alpha_q$ subunit polypeptide variant comprising a polypeptide with greater than 95% amino acid sequence identity to a sequence selected from the group consisting of SEQ ID Nos 1-26.

14. An isolated nucleic acid sequence encoding the G_q protein variant of claim 1.

15. An isolated nucleic acid sequence encoding the G_q protein variant of claim 11.

16. An isolated nucleic acid sequence encoding the G_q protein variant of claim 12.

17. An isolated nucleic acid sequence encoding a $G\alpha_q$ protein variant comprising a nucleic acid encoding a polypeptide with greater than 80% amino acid sequence identity to a sequence selected from the group consisting of SEQ ID Nos 1-26.

18. An isolated nucleic acid sequence encoding a $G\alpha_q$ protein variant comprising a nucleic acid encoding a polypeptide with greater than 90% amino acid sequence identity to a sequence selected from the group consisting of SEQ ID Nos 1-26.

19. An isolated nucleic acid sequence encoding a $G\alpha_q$ protein variant comprising a nucleic acid encoding a polypeptide with greater than 95% amino acid sequence identity to a sequence selected from the group consisting of SEQ ID Nos 1-26.

20. An antibody that selectively binds to the variant G_q alpha protein of claim 1, but not to the native G_q alpha protein.

21. An expression vector comprising the nucleic acid sequence of claim 14 operably linked to a promoter that functions in mammalian cells or *Xenopus* oocytes.

22. A host cell comprising the expression vector of claim 21.

23. A method for identifying a compound that modulates sensory signaling in sensory cells, the method comprising the steps of:

(i) contacting the compound with a cell expressing the G_q variant protein according to claim 1; and

(ii) determining the functional effect of said compound upon the G_q protein variant.

24. The method of claim 23, wherein said cell expressing said G_q variant protein is a transfected sensory cell.

25. The method of claim 23, wherein said cell expressing said G_q variant protein is a *Xenopus* oocyte.

26. The method of claim 23, wherein the functional effect is determined by measuring changes in intracellular cAMP, IP3 or Ca^{2+}.

27. The method of claim 23, wherein the functional effect is determined by measuring binding of a radiolabeled GTP to said variant G_q protein.

28. The method of claim 23, wherein the functional effect is determined by measuring changes in the electrical activity of the cells expressing said G_q variant protein.

29. The method of claim 23, wherein the functional effect is determined by observing modification of an intracellular effector enzyme.

30. The method of claim 23, wherein said G_q variant protein comprises sequences of a native G_q protein from a human or rodent.

31. The method of claim 23, wherein said compound is selected from the group consisting of agonists, antagonists, antibodies, small molecules, and proteins.

32. A method for identifying a compound that interacts with the G_q variant protein of claim 1, comprising the steps of:

(i) contacting said G_q variant protein with a test compound; and

(ii) detecting a binding interaction between said compound and said Gq protein variant.

33. The method of claim 32, wherein said G_q variant protein is linked to solid phase.

34. The method of claim 32, wherein said G_q variant protein is covalently linked to said solid phase.

35. The method of claim 32, wherein said compound is selected from the group consisting of agonists, antagonists, antibodies, small molecules, and proteins.

36. An artificial array of GPCRs functionally coupled to the G_q variant of claim 1, wherein said array is a model of a native arrangement of GPCRs.

37. The artificial array of claim 36, wherein said native arrangement is an arrangement of olfactory receptors (ORs) typically seen in a mammalian nose.

38. The artificial array of claim 36, wherein said native arrangement is an arrangement of taste receptors typically seen on a mammalian tongue.

39. The artificial array of claim 38, wherein said taste receptors include at least one type of taste receptor selected from the group consisting of bitter, sweet, salty, unami and sour taste receptors.